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GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 07:38:00 ; Search time 2207 Seconds
(without alignments)
1394.265 Million cell updates/sec

Title: US-09-895-298A-83
Perfect score: 190
Sequence: 1 MMNFQPPSKAWRASQMMTFF.....HDGSLDLRSRRSVQEGNPRA 190

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 4

Total number of hits satisfying chosen parameters: 19385028

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09895298/runat_06112002_160753_3581/app_query.fasta_1.327
-DB=EST -QFMT=fastap -SUFFIX=oligna.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=4 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09895298_@CGN_1_1_1716_@runat_06112002_160753_3581 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	190	100.0	807	12	BG184448	BG184448 RST3374 A
	2	181	95.3	691	10	AW582253	AW582253 QV4-ST021
	3	153	80.5	768	12	BG194960	BG194960 RST14018
	4	148	77.9	822	12	BG219307	BG219307 RST39061
	5	130	68.4	789	12	BG221275	BG221275 RST41079
	6	125	65.8	823	12	BG183902	BG183902 RST2815 A
	7	123	64.7	837	12	BG216071	BG216071 RST35885
c	8	112	58.9	447	13	BG982234	BG982234 CM4-CN008
c	9	110	57.9	594	10	AW469181	AW469181 hc78f11.x
	10	97	51.1	777	12	BG217799	BG217799 RST37513
	11	81	42.6	698	12	BF375244	BF375244 QV4-ST021
	12	78	41.1	871	12	BG198917	BG198917 RST18188
	13	74	38.9	307	12	BG187692	BG187692 RST6558 A
	14	70	36.8	415	14	BQ084432	BQ084432 K-EST0149
	15	70	36.8	482	14	BM773483	BM773483 K-EST0057
c	16	65	34.2	480	9	AI697014	AI697014 wc76h09.x
	17	61	32.1	268	12	BG184955	BG184955 RST3889 A
	18	55	28.9	529	13	BM432955	BM432955 1JEJ8B4.a
	19	55	28.9	758	12	BG198969	BG198969 RST18241
	20	54	28.4	810	12	BG217267	BG217267 RST36969
	21	50	26.3	398	14	BM773482	BM773482 K-EST0057
c	22	50	26.3	428	9	AI830044	AI830044 wj58f02.x
c	23	50	26.3	508	12	BF375243	BF375243 QV4-ST021
	24	50	26.3	777	9	AU138880	AU138880 AU138880
c	25	49	25.8	558	9	AI799626	AI799626 to74b03.x
c	26	45	23.7	846	12	BG202006	BG202006 RST21353
c	27	41	21.6	855	12	BG204090	BG204090 RST23484
	28	39	20.5	243	12	BG216765	BG216765 RST36460
	29	39	20.5	565	14	BQ552730	BQ552730 H4017G07-
	30	39	20.5	2721	11	AK016573	AK016573 Mus muscu
c	31	37	19.5	639	14	BM978431	BM978431 UI-CF-DU1
	32	36	18.9	359	14	BM750790	BM750790 K-EST0026
c	33	34	17.9	340	13	BG977333	BG977333 CM1-CI003
c	34	33	17.4	559	12	BF378919	BF378919 QV0-UM009
c	35	32	16.8	829	12	BG201350	BG201350 RST20811
	36	31	16.3	376	12	BE849364	BE849364 uw88h05.y
	37	31	16.3	491	10	AW913564	AW913564 uf54e02.y
	38	31	16.3	563	14	BM837518	BM837518 K-EST0113
c	39	28	14.7	585	10	AW469177	AW469177 hc78e12.x
c	40	27	14.2	324	10	AW869793	AW869793 MR4-SN007
c	41	27	14.2	327	10	BE183571	BE183571 CM0-HT067
c	42	25	13.2	303	12	BG205109	BG205109 RST24528
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	44	18	9.5	191	9	AA371314	AA371314 EST83087
c	45	16	8.4	361	10	BE002927	BE002927 QV4-BN009

ALIGNMENTS

RESULT 1
BG184448
LOCUS BG184448 807 bp mRNA linear EST 21-APR-2001
DEFINITION RST3374 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG184448
VERSION BG184448.1 GI:13706135
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 807)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
, Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith

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          ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
          ,J., Danzig,J. and Ducar,M.
  TITLE   Creation of genome-wide protein expression libraries using random
          activation of gene expression
  JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE 21227151
COMMENT   Contact: Scott J. Cain
          Athersys, Inc.
          3201 Carnegie Ave, Cleveland, OH 44115, USA
          Tel: 216 431 9900
          Fax: 216 361 9596
          Email: scain@athersys.com
          High quality sequence stop: 499.
FEATURES             Location/Qualifiers
     source          1. .807
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      211 a    195 c    178 g    222 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:              2.63e-192      Length:         807
Score:                  190.00         Matches:        190
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     12             Gaps:           0

US-09-895-298A-83 (1-190) x BG184448 (1-807)

Qy       1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
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Db      85 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 144

Qy      21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     145 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 204

Qy      41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     205 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 264

Qy      61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 324

Qy      81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 384

Qy     101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 444

Qy     121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 504

Qy     141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     505 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 564

Qy     161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     565 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 624
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Qy     181 ArgSerValGlnGluGlyAsnProArgAla 190
           ||||||||||||||||||||||||||||||
Db     625 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 654

RESULT 2
AW582253
LOCUS       AW582253                691 bp    mRNA    linear   EST 16-MAR-2000
DEFINITION  QV4-ST0212-120100-075-f09 ST0212 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW582253
VERSION     AW582253.1  GI:7257302
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 691)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV4&t2=QV4-ST0212-
            120100-075-f09&t3=2000-01-12&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 5
            High quality sequence stop: 667.
FEATURES             Location/Qualifiers
     source          1. .691
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="ST0212"
                     /dev_stage="Adult"
                     /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      179 a    167 c    157 g    188 t
ORIGIN

Alignment Scores:
Pred. No.:              9.22e-183      Length:         691
Score:                  181.00         Matches:        181
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            95.26%         Indels:         0
DB:                     10             Gaps:           0

US-09-895-298A-83 (1-190) x AW582253 (1-691)

Qy      10 AlaTrpArgAlaSerGlnMetMetThrPhePheIlePheLeuLeuPhePheProSerPhe 29
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      53 GCCTGGCGGGCCTCACAGATGATGACTTTCTTCATCTTCTTGCTCTTTTTCCCATCCTTC 112

Qy      30 ThrGlyValLeuCysThrLeuAlaIleThrIleTrpArgLeuLysProSerAlaAspCys 49
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     113 ACCGGGGTCTTGTGCACCCTGGCCATCACCATCTGGAGATTGAAGCCTTCAGCTGACTGT 172

Qy      50 GlyProPheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrpIleAspThrLeu 69
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     173 GGCCCTTTTCGAGGTCTGCCTCTCTTCATTCACTCCATCTACAGCTGGATCGACACCCTA 232
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```
Qy      70 SerThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleGlySerVal 89
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     233 AGTACACGGCCTGGCTACCTGTGGGTTGTTTGGATCTATCGGAACCTCATTGGAAGTGTG 292

Qy      90 HisPhePhePheIleLeuThrLeuIleValLeuIleIleThrTyrLeuTyrTrpGlnIle 109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     293 CACTTCTTTTTCATCCTCACCCTCATTGTGCTAATCATCACCTATCTTTACTGGCAGATC 352

Qy     110 ThrGluGlyArgLysIleMetIleArgLeuLeuHisGluGlnIleIleAsnGluGlyLys 129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     353 ACAGAGGGAAGGAAGATTATGATAAGGCTGCTCCATGAGCAGATCATTAATGAGGGCAAA 412

Qy     130 AspLysMetPheLeuIleGluLysLeuIleLysLeuGlnAspMetGluLysLysAlaAsn 149
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     413 GATAAAATGTTCCTGATAGAAAAATTGATCAAGCTGCAGGATATGGAGAAGAAAGCAAAC 472

Qy     150 ProSerSerLeuValLeuGluArgArgGluValGluGlnGlnGlyPheLeuHisLeuGly 169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     473 CCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTGGAGCAACAAGGCTTTTTGCATTTGGGG 532

Qy     170 GluHisAspGlySerLeuAspLeuArgSerArgArgSerValGlnGluGlyAsnProArg 189
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     533 GAACATGATGGCAGTCTTGACTTGCGATCTAGAAGATCAGTTCAAGAAGGTAATCCAAGG 592

Qy     190 Ala 190
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Db     593 GCC 595
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RESULT 3
BG194960
LOCUS BG194960 768 bp mRNA linear EST 21-APR-2001
DEFINITION RST14018 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG194960
VERSION BG194960.1 GI:13716535
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 768)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
, Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 469.
FEATURES Location/Qualifiers
source 1. .768
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 197 a 188 c 171 g 212 t
ORIGIN

Alignment Scores:
Pred. No.: 8.52e-153 Length: 768

Score: 153.00 Matches: 153
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 80.53% Indels: 0
DB: 12 Gaps: 0

US-09-895-298A-83 (1-190) x BG194960 (1-768)

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Qy       1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
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Db      85 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 144

Qy      21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     145 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 204

Qy      41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     205 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 264

Qy      61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     265 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 324

Qy      81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
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Db     325 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 384

Qy     101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 444

Qy     121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     445 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 504

Qy     141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeu 153
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Db     505 CTGCAGGATATGGAGAAGAAAGCCAACCCCAGCTCACTT 543
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RESULT 4
BG219307
LOCUS BG219307 822 bp mRNA linear EST 21-APR-2001
DEFINITION RST39061 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG219307
VERSION BG219307.1 GI:13745328
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 822)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
, Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 473.
FEATURES Location/Qualifiers
source 1. .822
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"

/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT 241 a 169 c 179 g 230 t 3 others
ORIGIN

Alignment Scores:

Pred. No.:	2.01e-147	Length:	822
Score:	148.00	Matches:	148
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	77.89%	Indels:	0
DB:	12	Gaps:	0

US-09-895-298A-83 (1-190) x BG219307 (1-822)

```
Qy      43 LeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHisSerIle 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79 TTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCACTCCATC 138

Qy      63 TyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrpIleTyr 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     139 TACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGGATCTAT 198

Qy      83 ArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeuIleIle 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     199 CGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTAATCATC 258

Qy     103 ThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeuHisGlu 122
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     259 ACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTCCATGAG 318

Qy     123 GlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLysLeuGln 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     319 CAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAGCTGCAG 378

Qy     143 AspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluValGluGln 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     379 GATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTGGAGCAA 438

Qy     163 GlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArgArgSer 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     439 CAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGAAGATCA 498

Qy     183 ValGlnGluGlyAsnProArgAla 190
           |||||||||||||||||||||||
Db     499 GTTCAAGAAGGTAATCCAAGGGCC 522
```

RESULT 5
BG221275
LOCUS BG221275 789 bp mRNA linear EST 21-APR-2001
DEFINITION RST41079 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG221275
VERSION BG221275.1 GI:13747296
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 789)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151

COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 533.
FEATURES Location/Qualifiers
source 1. .789
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT 191 a 194 c 171 g 226 t 7 others
ORIGIN

Alignment Scores:

Pred. No.:	3.3e-128	Length:	789
Score:	130.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	68.42%	Indels:	0
DB:	12	Gaps:	0

US-09-895-298A-83 (1-190) x BG221275 (1-789)

```
Qy      10 AlaTrpArgAlaSerGlnMetMetThrPhePheIlePheLeuLeuPhePheProSerPhe 29
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     215 GCCTGGCGGGCCTCACAGATGATGACTTTCTTCATCTTCTTGCTCTTTTTCCCATCCTTC 274

Qy      30 ThrGlyValLeuCysThrLeuAlaIleThrIleTrpArgLeuLysProSerAlaAspCys 49
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     275 ACCGGGGTCTTGTGCACCCTGGCCATCACCATCTGGAGATTGAAGCCTTCAGCTGACTGT 334

Qy      50 GlyProPheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrpIleAspThrLeu 69
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     335 GGCCCTTTTCGAGGTCTGCCTCTCTTCATTCACTCCATCTACAGCTGGATCGACACCCTA 394

Qy      70 SerThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleGlySerVal 89
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     395 AGTACACGGCCTGGCTACCTGTGGGTTGTTTGGATCTATCGGAACCTCATTGGAAGTGTG 454

Qy      90 HisPhePhePheIleLeuThrLeuIleValLeuIleIleThrTyrLeuTyrTrpGlnIle 109
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     455 CACTTCTTTTTCATCCTCACCCTCATTGTGCTAATCATCACCTATCTTTACTGGCAGATC 514

Qy     110 ThrGluGlyArgLysIleMetIleArgLeuLeuHisGluGlnIleIleAsnGluGlyLys 129
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     515 ACAGAGGGAAGGAAGATTATGATAAGGCTGCTCCATGAGCAGATCATTAATGAGGGCAAA 574

Qy     130 AspLysMetPheLeuIleGluLysLeuIle 139
           |||||||||||||||||||||||||||||
Db     575 GATAAAATGTTCCTGATAGAAAAATTGATC 604
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RESULT 6
BG183902
LOCUS BG183902 823 bp mRNA linear EST 21-APR-2001
DEFINITION RST2815 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG183902
VERSION BG183902.1 GI:13705589
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 823)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,

```
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 449.
FEATURES             Location/Qualifiers
     source          1. .823
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      211 a    203 c    180 g    229 t
ORIGIN

Alignment Scores:
Pred. No.:                7.58e-123     Length:          823
Score:                    125.00        Matches:         125
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              65.79%        Indels:          0
DB:                       12            Gaps:            0

US-09-895-298A-83 (1-190) x BG183902 (1-823)

Qy       1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     109 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 168

Qy      21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 228

Qy      41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     229 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 288

Qy      61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     289 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 348

Qy      81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     349 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 408

Qy     101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     409 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 468

Qy     121 HisGluGlnIleIle 125
           |||||||||||||||
Db     469 CATGAGCAGATCATC 483

RESULT 7
BG216071
LOCUS       BG216071                837 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST35885 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG216071
VERSION     BG216071.1  GI:13742220
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 837)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 537.
FEATURES             Location/Qualifiers
     source          1. .837
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      208 a    209 c    184 g    235 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:                1.06e-120     Length:          837
Score:                    123.00        Matches:         123
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              64.74%        Indels:          0
DB:                       12            Gaps:            0

US-09-895-298A-83 (1-190) x BG216071 (1-837)

Qy      39 ThrIleTrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPhe 58
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 ACCATCTGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTC 297

Qy      59 IleHisSerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpVal 78
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 ATTCACTCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTT 357

Qy      79 ValTrpIleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIle 98
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 GTTTGGATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATT 417

Qy      99 ValLeuIleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArg 118
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 GTGCTAATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGG 477

Qy     119 LeuLeuHisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeu 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 CTGCTCCATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTG 537

Qy     139 IleLysLeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArg 158
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     538 ATCAAGCTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGA 597

Qy     159 GluValGlu 161
```

```
          |||||||||
Db    598 GAGGTGGAG 606

RESULT 8
BG982234/c
LOCUS       BG982234                447 bp    mRNA    linear   EST 12-JUN-2001
DEFINITION  CM4-CN0089-130201-723-e04 CN0089 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG982234
VERSION     BG982234.1  GI:14384969
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 447)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM4&t2=CM4-CN0089-
            130201-723-e04&t3=2001-02-13&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 25
            High quality sequence stop: 447.
FEATURES              Location/Qualifiers
     source           1. .447
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone_lib="CN0089"
                      /dev_stage="Adult"
                      /note="Organ: colon_normal; Vector: puc18; Site_1: SmaI;
                      Site_2: SmaI; A mini-library was made by cloning products
                      derived from  ORESTES PCR (U.S. Letters Patent application
                      No. 196,716 -  Ludwig Institute for Cancer Research)
                      profiles into  the pUC 18 vector. Reverse transcription of
                      tissue mRNA and cDNA amplification were performed under
                      low stringency conditions."
BASE COUNT      114 a    107 c     95 g    131 t
ORIGIN

Alignment Scores:
Pred. No.:                3.1e-109      Length:          447
Score:                    112.00        Matches:         112
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              58.95%        Indels:          0
DB:                       13            Gaps:            0

US-09-895-298A-83 (1-190) x BG982234 (1-447)

Qy      79 ValTrpIleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIle 98
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     380 GTTTGGATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATT 321

Qy      99 ValLeuIleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArg 118
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     320 GTGCTAATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGG 261

Qy     119 LeuLeuHisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeu 138
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     260 CTGCTCCATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTG 201

Qy     139 IleLysLeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArg 158
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200 ATCAAGCTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGA 141

Qy     159 GluValGluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArg 178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     140 GAGGTGGAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGA 81

Qy     179 SerArgArgSerValGlnGluGlyAsnProArgAla 190
           ||||||||||||||||||||||||||||||||||||
Db      80 TCTAGAAGATCAGTTCAAGAAGGTAATCCAAGGGCC 45

RESULT 9
AW469181/c
LOCUS       AW469181                594 bp    mRNA    linear   EST 24-FEB-2000
DEFINITION  hc78f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2898861 3'
            similar to TR:O43284 O43284 LAK-4P. ;, mRNA sequence.
ACCESSION   AW469181
VERSION     AW469181.1  GI:7039287
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 404.
FEATURES              Location/Qualifiers
     source           1. .594
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2898861"
                      /clone_lib="NCI_CGAP_Gas4"
                      /tissue_type="poorly differentiated adenocarcinoma with
                      signet ring cell features"
                      /lab_host="DH10B"
                      /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
                      Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.69 kb. Life Technologies catalog #:
                      11549-011"
BASE COUNT      161 a    139 c    108 g    186 t
ORIGIN

Alignment Scores:
Pred. No.:                5.73e-107     Length:          594
Score:                    110.00        Matches:         110
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              57.89%        Indels:          0
DB:                       10            Gaps:            0

US-09-895-298A-83 (1-190) x AW469181 (1-594)

Qy      81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    582 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTA 523

Qy    101 IleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    522 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCTC 463

Qy    121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    462 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 403

Qy    141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    402 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 343

Qy    161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    342 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 283

Qy    181 ArgSerValGlnGluGlyAsnProArgAla 190
          ||||||||||||||||||||||||||||||
Db    282 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 253

RESULT 10
BG217799
LOCUS       BG217799                 777 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST37513 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG217799
VERSION     BG217799.1  GI:13743820
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 512.
FEATURES             Location/Qualifiers
     source          1. .777
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      196 a    193 c    173 g    214 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:                5.9e-93       Length:          777
Score:                    97.00         Matches:         178
Percent Similarity:       98.89%        Conservative:    0
Best Local Similarity:    98.89%        Mismatches:      1
Query Match:              51.05%        Indels:          2
DB:                       12            Gaps:            0

US-09-895-298A-83 (1-190) x BG217799 (1-777)

Qy      1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 144

Qy     21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCATC 204

Qy     41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    205 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 264

Qy     61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    265 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGG 324

Qy     81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIle-ValLe 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    325 ATCTATCGGAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCAC-TGTGCT 383

Qy    100 uIleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLe 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 AATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGGAAGATTATGATAAGGCTGCT 443

Qy    120 uHisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLy 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 CCATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAA 503

Qy    140 sLeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVa 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    504 GCTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGT 563

Qy    160 lGluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSer 179
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    564 GGAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCT 621

RESULT 11
BF375244
LOCUS       BF375244                 698 bp    mRNA    linear   EST 24-NOV-2000
DEFINITION  QV4-ST0212-261199-045-c09 ST0212 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF375244
VERSION     BF375244.1  GI:11337269
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV4&t2=QV4-ST0212-
            261199-045-c09&t3=1999-11-26&t4=1)
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```
          Seq primer: puc 18 forward
          High quality sequence start: 14
          High quality sequence stop: 36.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="ST0212"
                     /dev_stage="Adult"
                     /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      177 a    173 c    164 g    184 t
ORIGIN

Alignment Scores:
Pred. No.:              6.58e-76       Length:         698
Score:                  81.00          Matches:        81
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            42.63%         Indels:         0
DB:                     12             Gaps:           0

US-09-895-298A-83 (1-190) x BF375244 (1-698)

Qy      48 AspCysGlyProPheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrpIleAsp 67
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     176 GACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCACTCCATCTACAGCTGGATCGAC 235

Qy      68 ThrLeuSerThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleGly 87
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     236 ACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGGATCTATCGGAACCTCATTGGA 295

Qy      88 SerValHisPhePhePheIleLeuThrLeuIleValLeuIleIleThrTyrLeuTyrTrp 107
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     296 AGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTAATCATCACCTATCTTTACTGG 355

Qy     108 GlnIleThrGluGlyArgLysIleMetIleArgLeuLeuHisGluGlnIleIleAsnGlu 127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     356 CAGATCACAGAGGGAAGGAAGATCATGATCAGGCTGCTCCATGAGCAGATCATTAATGAG 415

Qy     128 Gly 128
           |||
Db     416 GGC 418

RESULT 12
BG198917
LOCUS       BG198917                871 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST18188 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG198917
VERSION     BG198917.1  GI:13720604
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 498.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      252 a    186 c    185 g    246 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:              1.33e-72       Length:         871
Score:                  78.00          Matches:        146
Percent Similarity:     97.33%         Conservative:   0
Best Local Similarity:  97.33%         Mismatches:     2
Query Match:            41.05%         Indels:         4
DB:                     12             Gaps:           0

US-09-895-298A-83 (1-190) x BG198917 (1-871)

Qy      43 LeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHisSerIle 62
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     117 TTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCACTCCATC 176

Qy      63 TyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrpIleTyr 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     177 TACAGCTGGATCGACACCCTAAGTACACGGCCTGGCTACCTGTGGGTTGTTTGGATCTAT 236

Qy      83 Arg-AsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeuIleIl 102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     237 TG-GAACCTCATTGGAAGTGTGCACTTCTTTTTCATCCTCACCCTCATTGTGCTAATCAT 295

Qy     102 eThrTyrLeuTyrTrpGlnIleThrGluGly-ArgLysIleMetIleArgLeuLeuHisG 122
           |||||||||||||||||||||||||||||   ||| ||||||||||||||||||||||||||
Db     296 CACCTATCTTTACTGGCAGATCACAGA-GGAAAGGAAGATTATGATAAGGCTGCTCCATG 354

Qy     122 luGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLysLeuG 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 AGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAGCTGC 414

Qy     142 lnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluValGluG 162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     415 AGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTGGAGC 474

Qy     162 lnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArgArgS 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     475 AACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGAAGAT 534

Qy     182 erValGlnGluGlyAsnProArgAla 190
           |||||||||||||||||||||||||
Db     535 CAGTTCAAGAAGGTAATCCAAGGGCC 560

RESULT 13
BG187692
LOCUS       BG187692                307 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST6558 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG187692
VERSION     BG187692.1  GI:13709251
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 307)
```

AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 307.

FEATURES Location/Qualifiers
source 1. .307
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 58 a 98 c 56 g 95 t
ORIGIN

Alignment Scores:

Pred. No.:	8.36e-69	Length:	307
Score:	74.00	Matches:	74
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	38.95%	Indels:	0
DB:	12	Gaps:	0

US-09-895-298A-83 (1-190) x BG187692 (1-307)

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Qy       1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      85 ATGATGAATTTCCAGCCTCCGAGCAAAGCCTGGCGGGCCTCACAGATGATGACTTTCTTC 144

Qy      21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     145 ATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCCTGTGCACCCTGGCCATCACCATC 204

Qy      41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     205 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTCAC 264

Qy      61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGly 74
          ||||||||||||||||||||||||||||||||||||||||||
Db     265 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCCTGGC 306
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RESULT 14
BQ084432
LOCUS BQ084432 415 bp mRNA linear EST 04-APR-2002
DEFINITION K-EST0149711 S14K402 Homo sapiens cDNA clone S14K402-77-A05 5', mRNA sequence.
ACCESSION BQ084432
VERSION BQ084432.1 GI:19944432
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 77 row: A column: 05
High quality sequence stop: 415.

FEATURES Location/Qualifiers
source 1. .415
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S14K402-77-A05"
/clone_lib="S14K402"
/cell_line="K402"
/lab_host="Top10F'"
/note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 136 a 74 c 101 g 104 t
ORIGIN

Alignment Scores:

Pred. No.:	2.16e-64	Length:	415
Score:	70.00	Matches:	70
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	36.84%	Indels:	0
DB:	14	Gaps:	0

US-09-895-298A-83 (1-190) x BQ084432 (1-415)

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Qy     121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 60

Qy     141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 120

Qy     161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 180

Qy     181 ArgSerValGlnGluGlyAsnProArgAla 190
           ||||||||||||||||||||||||||||||
Db     181 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 210
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RESULT 15
BM773483
LOCUS BM773483 482 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0057945 S14K402 Homo sapiens cDNA clone S14K402-27-D11 5', mRNA sequence.
ACCESSION BM773483
VERSION BM773483.1 GI:19103098
KEYWORDS EST.
SOURCE human.

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 482)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 27  row: D  column: 11
            High quality sequence stop: 482.
FEATURES             Location/Qualifiers
     source          1. .482
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S14K402-27-D11"
                     /clone_lib="S14K402"
                     /cell_line="K402"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT      164 a     83 c    112 g    123 t
ORIGIN

Alignment Scores:
Pred. No.:                2.52e-64        Length:          482
Score:                    70.00           Matches:         70
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              36.84%          Indels:          0
DB:                       14              Gaps:            0

US-09-895-298A-83 (1-190) x BM773483 (1-482)

Qy    121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCTGATAGAAAAATTGATCAAG 60

Qy    141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTG 120

Qy    161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GAGCAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGA 180

Qy    181 ArgSerValGlnGluGlyAsnProArgAla 190
          ||||||||||||||||||||||||||||||
Db    181 AGATCAGTTCAAGAAGGTAATCCAAGGGCC 210

Search completed: November  9, 2002, 09:08:43

Job time : 2214 secs
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